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TECH CENTER 1600/2900

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-- SEQUENCE LISTING

<110> Dahlqvist, Andres
Stahl, Ulf
Lenman, Marit
Banas, Antoni
Ronne, Hans

<120> A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant DNA molecules encoding these enzymes

<130> BASFnae337799PCT1-15

<140> US 09/537,710

<141> 2000-03-30

<150> EP 99106656.4

<151> 1999-04-01

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DI

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
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<211> 671

<212> PRT

<213> Arabidopsis thaliana

<400> 6

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Glu	Ser	Ser	Lys	Ser	His	His	Lys	Lys	Ser	Asn	Gly	Gly	Gly	Lys	Trp
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Ser	Cys	Ile	Asp	Ser	Cys	Cys	Trp	Phe	Ile	Gly	Cys	Val	Cys	Val	Thr
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Trp	Trp	Phe	Leu	Leu	Phe	Leu	Tyr	Asn	Ala	Met	Pro	Ala	Ser	Phe	Pro
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Gln	Tyr	Val	Thr	Glu	Arg	Ile	Thr	Gly	Pro	Leu	Pro	Asp	Pro	Pro	Gly

10

85

90

95

Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe
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Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
115 120 125

Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
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Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
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165 170 175

Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
180 185 190

Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
195 200 205

Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
210 215 220

Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
225 230 235 240

Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
245 250 255

Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
260 265 270

Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala
275 280 285

Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
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Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
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Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
325 330 335

His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
340 345 350

Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
355 360 365

Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
370 375 380

Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
385 390 395 400

DI

Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
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 Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
 420 425 430
 Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
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 Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
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 Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
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 545 550 555 560
 Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
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 Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
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 595 600 605
 His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
 610 615 620
 Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
 625 630 635 640
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 <213> Zea mays

<220>
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<221> Unsure

<222> 1..643

<223> n= a or g or c or t/u

<221> Unsure

<222> 1...643

<223> Xaa = unknown

<400> 7

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Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly	
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tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg	144
Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val	
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Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly	
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Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile	
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gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt	288
Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly	
85 90 95	
ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa	336
Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys	
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Leu Lys Leu Xaa Pro Met Gly Ser Xaa Arg Ser Ala Asp Pro Phe Ile	
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Ala Phe Gln Ser Val Leu	
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<210> 8

<211> 115

<212> PRT

<213> Zea mays

<400> 8

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 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
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 Leu Lys Leu
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<210> 9

<211> 616

<212> DNA

<213> *Neurospora crassa*

<220>

<221> Unsure

<222> 1..616

<223> n= a or g or c or t/u

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 tttagatgac gatcgatacg actttgactn aggggcacat tgaccacggg gtgattttgg 240
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<210> 10

<211> 1562

<212> DNA

<213> *Arabidopsis thaliana*

<400> 10

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<210> 11

<211> 3896

<212> DNA

<213> Arabidopsis thaliana

<400> 11

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<211> 709

<212> DNA

<213> *Lycopersicon esculentum*

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<210> 13
 <211> 623
 <212> PRT
 <213> Schizosaccharomyces pombe

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 Ser Glu Gln Pro Ser Ala Ser Glu Thr Gln Ser Val Ser Asn Lys Ser
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 Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile
 50 55 60
 Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala
 65 70 75 80
 Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser
 85 90 95
 Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe
 100 105 110
 Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly
 115 120 125
 Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser
 130 135 140
 Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu
 145 150 155 160
 Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu
 165 170 175
 Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys
 180 185 190
 Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys
 195 200 205
 Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe
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 225 230 235 240
 Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg
 245 250 255
 Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu

260 265 270
 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
 275 280 285
 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
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 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn
 305 310 315 320
 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
 325 330 335
 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
 340 345 350
 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
 355 360 365
 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro
 370 375 380
 Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
 385 390 395 400
 Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
 405 410 415
 Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
 420 425 430
 Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala
 435 440 445
 Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
 450 455 460
 Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
 465 470 475 480
 Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr
 485 490 495
 Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp
 500 505 510
 Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr
 515 520 525
 Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr
 530 535 540
 Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys
 545 550 555 560
 His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu
 565 570 575

DI

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn
610 615 620

<210> 14

<211> 432

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val
1 5 10 15

Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr
20 25 30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg
35 40 45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu
50 55 60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp
65 70 75 80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met
85 90 95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly
100 105 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr
115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val
130 135 140

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu
145 150 155 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro
165 170 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu
180 185 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His
195 200 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro
210 215 220

Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro

225 230 235 240
 Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr
 245 250 255
 Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg
 260 265 270
 Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His
 275 280 285
 Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala
 290 295 300
 Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val
 305 310 315 320
 Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr
 325 330 335
 Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro
 340 345 350
 Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile
 355 360 365
 Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala
 370 375 380
 Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His
 385 390 395 400
 Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln
 405 410 415
 Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
 420 425 430

<210> 15
 <211> 552
 <212> PRT
 <213> Arabidopsis thaliana

<400> 15
 Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala
 1 5 10 15
 Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr
 20 25 30
 Glu Phe His Gly Asp Tyr Ser Lys Leu Ser Gly Ile Ile Ile Pro Gly
 35 40 45
 Phe Ala Ser Thr Gln Leu Arg Ala Trp Ser Ile Leu Asp Cys Pro Tyr
 50 55 60

Thr Pro Leu Asp Phe Asn Pro Leu Asp Leu Val Trp Leu Asp Thr Thr
 65 70 75 80
 Lys Leu Leu Ser Ala Val Asn Cys Trp Phe Lys Cys Met Val Leu Asp
 85 90 95
 Pro Tyr Asn Gln Thr Asp His Pro Glu Cys Lys Ser Arg Pro Asp Ser
 100 105 110
 Gly Leu Ser Ala Ile Thr Glu Leu Asp Pro Gly Tyr Ile Thr Gly Pro
 115 120 125
 Leu Ser Thr Val Trp Lys Glu Trp Leu Lys Trp Cys Val Glu Phe Gly
 130 135 140
 Ile Glu Ala Asn Ala Ile Val Ala Val Pro Tyr Asp Trp Arg Leu Ser
 145 150 155 160
 Pro Thr Lys Leu Glu Glu Arg Asp Leu Tyr Phe His Lys Leu Lys Leu
 165 170 175
 Thr Phe Glu Thr Ala Leu Lys Leu Arg Gly Gly Pro Ser Ile Val Phe
 180 185 190
 Ala His Ser Met Gly Asn Asn Val Phe Arg Tyr Phe Leu Glu Trp Leu
 195 200 205
 Arg Leu Glu Ile Ala Pro Lys His Tyr Leu Lys Trp Leu Asp Gln His
 210 215 220
 Ile His Ala Tyr Phe Ala Val Gly Ala Pro Leu Leu Gly Ser Val Glu
 225 230 235 240
 Ala Ile Lys Ser Thr Leu Ser Gly Val Thr Phe Gly Leu Pro Val Ser
 245 250 255
 Glu Gly Thr Ala Arg Leu Leu Ser Asn Ser Phe Ala Ser Ser Leu Trp
 260 265 270
 Leu Met Pro Phe Ser Lys Asn Cys Lys Gly Asp Asn Thr Phe Trp Thr
 275 280 285
 His Phe Ser Gly Gly Ala Ala Lys Lys Asp Lys Arg Val Tyr His Cys
 290 295 300
 Asp Glu Glu Glu Tyr Gln Ser Lys Tyr Ser Gly Trp Pro Thr Asn Ile
 305 310 315 320
 Ile Asn Ile Glu Ile Pro Ser Thr Ser Ala Arg Glu Leu Ala Asp Gly
 325 330 335
 Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met
 340 345 350
 Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile
 355 360 365
 Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro
 370 375 380

Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val
 385 390 395 400
 Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe
 405 410 415
 Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile
 420 425 430
 Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val
 435 440 445
 Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His
 450 455 460
 Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr
 465 470 475 480
 Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His
 485 490 495
 Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly
 500 505 510
 Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile
 515 520 525
 Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val
 530 535 540
 Trp Glu Leu Asp Lys Ser Gly Tyr
 545 550

<210> 16
 <211> 661
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 16
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe

100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655
 Met Pro Phe Pro Met
 660

<210> 17
 <211> 387
 <212> PRT
 <213> Arabidopsis thaliana

<400> 17
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 1 5 10 15
 Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val

20 25 30
 Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp
 35 40 45
 Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg
 50 55 60
 Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp
 65 70 75 80
 Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser
 85 90 95
 Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser
 100 105 110
 Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val
 115 120 125
 Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu
 130 135 140
 Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp
 145 150 155 160
 Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro
 165 170 175
 Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu His Phe
 180 185 190
 Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe
 195 200 205
 Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr
 210 215 220
 Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu
 225 230 235 240
 Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro
 245 250 255
 Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro
 260 265 270
 Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile
 275 280 285
 Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu
 290 295 300
 Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly
 305 310 315 320
 Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe
 325 330 335

Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn
 340 345 350
 Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu
 355 360 365
 Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu
 370 375 380
 Lys Glu Ile
 385

<210> 18
 <211> 389
 <212> PRT
 <213> Arabidopsis thaliana

<400> 18
 Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro
 1 5 10 15
 Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala
 20 25 30
 Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp
 35 40 45
 Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly
 50 55 60
 Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala
 65 70 75 80
 Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile
 85 90 95
 Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu
 100 105 110
 Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
 115 120 125
 Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile
 130 135 140
 Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
 145 150 155 160
 Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys
 165 170
 Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
 180 185 190
 Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met
 195 200 205
 Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly

210 215 220
 Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
 225 230 235 240
 Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
 245 250 255
 Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
 260 265 270
 Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
 275 280 285
 Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
 290 295 300
 Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
 305 310 315 320
 Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
 325 330 335
 Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
 340 345 350
 Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val
 355 360 365
 Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser
 370 375 380
 Gly Ile Phe Glu Trp
 385

<210> 19
 <211> 1986
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (1983)

<400> 19
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 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30
 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45
 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190

gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205

gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg 672
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220

ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac 720
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240

ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc 768
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255

gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att 816
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270

ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt 864
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285

gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag 912
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300

gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta 960
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320

att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg 1008
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335

gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt 1056
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350

aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc 1104
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365

gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc 1152
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca 1200
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca 1248
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct 1296
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430

tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

atg ccc ttc cca atg taa 1986
 Met Pro Phe Pro Met
 660

<210> 20
 <211> 661
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 20
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser.
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe

85

90

95

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
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ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432
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Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile				
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Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile				
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Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met				
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 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
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 Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
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 cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215
 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
 20 25 30
 gaa tct tcc aaa tcc cac cat aag naa tcg aac gga gga ggg aag tgg 263
 Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Gly Lys Trp
 35 40 45
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 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
 50 55 60
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 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
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 Leu Lys Leu Xaa Pro Met Gly Ser Xaa Arg Ser Ala Asp Pro Phe Ile
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 Ala Phe Gln Ser Val Leu
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 35 40 45
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
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DI

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DI

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709
